



1/4

SEQUENCE LISTING

RECEIVED

AUG 31 2000

TECH CENTER 1600/2900

<110> Williamson, Mark

<120> MDA-9 AND USES THEREOF

<130> 07334-122001

<140> US 09/531,369

<141> 2000-03-21

<150> US 60/125,759

<151> 1999-03-23

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2068

<212> DNA

<213> Homo sapiens

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Met Ser Leu Tyr Pro Ser Leu Glu Asp Leu Lys Val
1 5 10

gac aaa gta att cag gct caa act gct ttt tct gca aac cct gcc aat 159
Asp Lys Val Ile Gln Ala Gln Thr Ala Phe Ser Ala Asn Pro Ala Asn
15 20 25

cca gca att ttg tca gaa gct tct gct cct atc cct cac gat gga aat 207
Pro Ala Ile Leu Ser Glu Ala Ser Ala Pro Ile Pro His Asp Gly Asn
30 35 40

ctc tat ccc aga ctg tat cca gag ctc tct caa tac atg ggg ctg agt 255
Leu Tyr Pro Arg Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu Ser
45 50 55 60

tta aat gaa gaa gaa ata cgt gca aat gtg gcc gtg gtt tct ggt gca 303
Leu Asn Glu Glu Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly Ala
65 70 75

cca ctt cag ggg cag ttg gta gca aga cct tcc agt ata aac tat atg 351
Pro Leu Gln Gly Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr Met
80 85 90

gtg gct cct gta act ggt aat gat gtt gga att cgt aga gca gaa att 399
Val Ala Pro Val Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu Ile
95 100 105

aag caa ggg att cgt gaa gtc att ttg tgt aag gat caa gat gga aaa 447
Lys Gln Gly Ile Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly Lys
110 115 120

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TECH CENTER 1600/2900

att gga ctc agg ctt aaa tca ata gat aat ggt ata ttt gtt cag cta 495
 Ile ly Leu Arg Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln Leu
 125 130 135 140

gtc cag gct aat tct cca gcc tca ttg gtt ggt ctg aga ttt ggg gac 543
 Val Gln Ala Asn Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly Asp
 145 150 155

caa gta ctt cag atc aat ggt gaa aac tgt gca gga tgg agc tct gat 591
 Gln Val Leu Gln Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser Asp
 160 165 170

aaa gcg cac aag gtg ctc aaa cag gct ttt gga gag aag att acc atg 639
 Lys Ala His Lys Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr Met
 175 180 185

acc att cgt gac agg ccc ttt gaa cgg acg att acc atg cat aag gat 687
 Thr Ile Arg Asp Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys Asp
 190 195 200

agc act gga cat gtt ggt ttt atc ttt aaa aat gga aaa ata aca tcc 735
 Ser Thr Gly His Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr Ser
 205 210 215 220

ata gtg aaa gat agc tct gca gcc aga aat ggt ctt ctc acg gaa cat 783
 Ile Val Lys Asp Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu His
 225 230 235

aac atc tgt gaa atc aat gga cag aat gtc att gga ttg aag gac tct 831
 Asn Ile Cys Glu Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp Ser
 240 245 250

caa att gca gac ata ctg tca aca tct ggg act gta gtt act att aca 879
 Gln Ile Ala Asp Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile Thr
 255 260 265

atc atg cct gct ttt atc ttt gaa cat att att aag cgg atg gca cca 927
 Ile Met Pro Ala Phe Ile Phe Glu His Ile Ile Lys Arg Met Ala Pro
 270 275 280

agc att atg aaa agc cta atg gac cac acc att cct gag gtt t 970
 Ser Ile Met Lys Ser Leu Met Asp His Thr Ile Pro Glu Val
 285 290 295

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 ctgtattatg cacgtgaagc cttcccggag ccagcgagca tatgctgcat gaggaccttt 1090
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<212> PRT
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35 40 45
Leu Tyr Pro Glu Leu Ser Gln Tyr Met Gly Leu Ser Leu Asn Glu Glu
50 55 60
Glu Ile Arg Ala Asn Val Ala Val Val Ser Gly Ala Pro Leu Gln Gly
65 70 75 80
Gln Leu Val Ala Arg Pro Ser Ser Ile Asn Tyr Met Val Ala Pro Val
85 90 95
Thr Gly Asn Asp Val Gly Ile Arg Arg Ala Glu Ile Lys Gln Gly Ile
100 105 110
Arg Glu Val Ile Leu Cys Lys Asp Gln Asp Gly Lys Ile Gly Leu Arg
115 120 125
Leu Lys Ser Ile Asp Asn Gly Ile Phe Val Gln Leu Val Gln Ala Asn
130 135 140
Ser Pro Ala Ser Leu Val Gly Leu Arg Phe Gly Asp Gln Val Leu Gln
145 150 155 160
Ile Asn Gly Glu Asn Cys Ala Gly Trp Ser Ser Asp Lys Ala His Lys
165 170 175
Val Leu Lys Gln Ala Phe Gly Glu Lys Ile Thr Met Thr Ile Arg Asp
180 185 190
Arg Pro Phe Glu Arg Thr Ile Thr Met His Lys Asp Ser Thr Gly His
195 200 205
Val Gly Phe Ile Phe Lys Asn Gly Lys Ile Thr Ser Ile Val Lys Asp
210 215 220
Ser Ser Ala Ala Arg Asn Gly Leu Leu Thr Glu His Asn Ile Cys Glu
225 230 235 240
Ile Asn Gly Gln Asn Val Ile Gly Leu Lys Asp Ser Gln Ile Ala Asp
245 250 255
Ile Leu Ser Thr Ser Gly Thr Val Val Thr Ile Thr Ile Met Pro Ala
260 265 270
Phe Ile Phe Glu His Ile Ile Lys Arg Met Ala Pro Ser Ile Met Lys
275 280 285
Ser Leu Met Asp His Thr Ile Pro Glu Val
290 295

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<211> 894
<212> DNA
<213> Homo sapiens

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cacgatggaa atctctatcc cagactgtat ccagagctct ctcaatacat ggggctgagt 180
ttaaatgaag aagaaatacg tgcaaatgtg gccgtggttt ctggtgcacc acttcagggg 240
cagttggtag caagaccttc cagtataaac tatatggtgg ctctgtaac tggtaatgat 300
gttggaattc gtagagcaga aattaagcaa gggattcgtg aagtcatttt gtgtaaggat 360
caagatggaa aaattggact caggcttaaa tcaatagata atggtatatt tggtcagcta 420
gtccaggcta attctccagc ctcattgggtt ggtctgagat ttggggacca agtacttcag 480

A1 concu

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gcttttggag	agaagattac	catgaccatt	cgtgacaggc	cctttgaacg	gacgattacc	600
atgcataagg	atagcactgg	acatgttggt	tttatcttta	aaaatggaaa	aataacatcc	660
atagtgaag	atagctctgc	agccagaaat	ggtcttctca	cggaacataa	catctgtgaa	720
atcaatggac	agaatgtcat	tggattgaag	gactctcaaa	ttgcagacat	actgtcaaca	780
tctgggactg	tagttactat	tacaatcatg	cctgctttta	tctttgaaca	tattattaag	840
cggatggcac	caagcattat	gaaaagccta	atggaccaca	ccattcctga	ggtt	894
